

WE CLAIM:

1. A method for carbazole biodegradation comprising the step of:  
contacting a microbial strain capable of expressing a carbazole degradation trait constitutively with carbazole, resulting in degradation of at least a portion of said carbazole.
2. A method in accordance with Claim 1, wherein said microbial strain is *Sphingomonas sp.* ATCC No. BAA-487.
3. A method in accordance with Claim 1, wherein said carbazole is disposed in a material selected from the group consisting of shale oil, crude oil, petroleum products, coal tar and mixtures thereof.
4. A method for removal of nitrogen from nitrogen-containing fossil fuels comprising the step of:  
contacting at least one of said fossil fuels with a microbial strain capable of expressing a carbazole degradation trait constitutively, resulting in removal of at least a portion of said nitrogen.

5. A method in accordance with Claim 4, wherein said fossil fuels are selected from the group consisting of shale oil, crude oil, petroleum products, coal tar and mixtures thereof.

6. A method in accordance with Claim 4, wherein said microbial strain is *Sphingomonas sp.* ATCC No. BAA-487.

7. A method in accordance with Claim 4, wherein said nitrogen is a component of carbazole disposed in said fossil fuel.

8. A method for selective cleavage of C-N bonds comprising the steps of:

combining genes that encode for at least one enzyme suitable for conversion of carbazole to 2-aminobiphenyl-2,3-diol with a gene encoding an amidase suitable for selectively cleaving a C-N bond in said 2-aminobiphenyl-2,3-diol, forming an operon that encodes for cleavage of both C-N bonds of said carbazole;

inserting said operon into a host culture; and

contacting said host culture with said carbazole, resulting in selective cleavage of said C-N bonds.

9. A method in accordance with Claim 8, wherein said genes that encode for at least one enzyme suitable for conversion of said carbazole to said 2-aminobiphenyl-2,3-diol are a *carAa* gene, a *carAc* gene and a *carAd* gene of *Sphingomonas sp.* ATCC No. BAA-487.

10. A method in accordance with Claim 8, wherein said host culture is *Sphingomonas sp.* ATCC No. BAA-487.

11. A method in accordance with Claim 8, wherein said host culture is *E. coli*.

12. A method in accordance with Claim 8, wherein said genes that encode for at least one enzyme suitable for conversion of said carbazole to said 2-aminobiphenyl-2,3-diol are a *carAa* gene and a *carAc* gene from *Sphingomonas sp.* ATCC No. BAA-487 and a *carAd* (SEQ ID NO. 3) gene from *Pseudomonas resinovorans* CA10.

13. A method in accordance with Claim 8, wherein said gene encoding said amidase is an *amdA* (SEQ ID NO. 4) gene from *Rhodococcus erythropolis* MP50.

14. A method in accordance with Claim 8, wherein said gene encoding said amidase is a *triA* gene from *Pseudomonas sp.* NRRL B-12227.

15. A method in accordance with Claim 8, wherein said host culture is selected from the group consisting of *E. coli*, *Rhodococcus erythropolis*, *Sphingomonas sp.*, *Thermus thermophilus* and mixtures thereof.

16. A method in accordance with Claim 8, wherein said gene encoding said amidase is a derivative gene of a gene selected from the group consisting of an *amdA* (SEQ ID NO. 4) gene from *Rhodococcus erythropolis* MP50 and a *triA* gene from *Pseudomonas sp.* NRRL B-12227.

17. An operon that encodes for enzymes capable of selectively cleaving both C-N bonds in carbazole.

18. An operon in accordance with Claim 17 comprising a gene encoding amidase capable of cleaving said C-N bonds in 2-aminobiphenyl-2,3-diol.

19. An operon in accordance with Claim 17 comprising a *carAa* gene and a *carAc* gene from *Sphingomonas sp.* ATCC No. BAA-487 and a *carAd* gene from at least one of said *Sphingomonas sp.* ATCC No. BAA-487 and *Pseudomonas resinovorans* CA10.

20. A bacterial culture comprising:  
a biochemical pathway suitable for selective cleavage of C-N bonds.

21. A bacterial culture in accordance with Claim 20, wherein said biochemical pathway comprises an operon comprising a *carAa* gene and a *carAc* gene from *Sphingomonas sp.* ATCC No. BAA-487 and a *carAd* gene from at least one of said *Sphingomonas sp.* ATCC No. BAA-487 and *Pseudomonas resinovorans* CA10.

22. A DNA sequence comprising:  
at least one *carA* gene sequence of *Sphingomonas sp.* GenBank Accession No. AF442494 and at least one amidase gene sequence.

23. A biologically pure culture of mutant *Sphingomonas sp.* strain ATCC No. BAA-487.

24. A biologically pure culture of nitrogen selective mutant *Sphingomonas sp.* strain ATCC No. BAA-487 capable of selectively reducing the nitrogen content of nitrogen-containing fossil fuels.